

SEQUENCE LISTING

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 Kentaro ENJO
 Sadao KUROMITSU

<120> Method for screening an agent for treating renal failure

<130> Q85059

<150> PCT/JP03/012967

<151> 2003-10-09

<150> JP2002-298958

<151> 2002-10-11

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 993

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(990)

<223> inventor:Enjo, Kentaro; Kuromitsu, Sadao

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ctg gaa aag tac tac ctt tcc att ttt tat ggg att gag ttc gtt gtg	96
Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe Val Val	
20 25 30	

gga gtc ctt gga aat acc att gtt gtt tac ggc tac atc ttc tct ctg	144
Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe Ser Leu	
35 40 45	

aag aac tgg aac agc agt aat att tat ctc ttt aac ctc tct gtc tct	192
Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser Val Ser	
50 55 60	

gac tta gct ttt ctg tgc acc ctc ccc atg ctg ata agg agt tat gcc	240
Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser Tyr Ala	
65 70 75 80	

aat gga aac tgg ata tat gga gac gtg ctc tgc ata agc aac cga tat	288
Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr	
85 90 95	

gtg ctt cat gcc aac ctc tat acc agc att ctc ttt ctc act ttt atc	336
Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile	
100 105 110	

agc ata gat cga tac ttg ata att aag tat cct ttc cga gaa cac ctt	384
Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu His Leu	
115 120 125	
ctg caa aag aaa gag ttt gct att tta atc tcc ttg gcc att tgg gtt	432
Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile Trp Val	
130 135 140	
tta gta acc tta gag tta cta ccc ata ctt ccc ctt ata aat cct gtt	480
Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn Pro Val	
145 150 155 160	
ata act gac aat ggc acc acc tgt aat gat ttt gca agt tct gga gac	528
Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser Gly Asp	
165 170 175	
ccc aac tac aac ctc att tac agc atg tgt cta aca ctg ttg ggg ttc	576
Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu Gly Phe	
180 185 190	
ctt att cct ctt ttt gtg atg tgt ttc ttt tat tac aag att gct ctc	624
Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile Ala Leu	
195 200 205	
ttc cta aag cag agg aat agg cag gtt gct act gct ctg ccc ctt gaa	672
Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro Leu Glu	
210 215 220	
aag cct ctc aac ttg gtc atc atg gca gtg gta atc ttc tct gtg ctt	720
Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser Val Leu	
225 230 235 240	
ttt aca ccc tat cac gtc atg cgg aat gtg agg atc gct tca cgc ctg	768
Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser Arg Leu	
245 250 255	
ggg agt tgg aag cag tat cag tgc act cag gtc gtc atc aac tcc ttt	816
Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn Ser Phe	
260 265 270	
tac att gtg aca cgg gct ttg ggc ttt ctg aac agt gtc atc aac cct	864
Tyr Ile Val Thr Arg Ala Leu Gly Phe Leu Asn Ser Val Ile Asn Pro	
275 280 285	
gtc ttc tat ttt ctt ttg gga gat cac ttc agg gac atg ctg atg aat	912
Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu Met Asn	
290 295 300	
caa ctg aga cac aac ttc aaa tcc ctt aca tcc ttt agc aga tgg gct	960
Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg Trp Ala	
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cat gaa ctc cta ctt tca ttc aga gaa aag tga	993
His Glu Leu Leu Leu Ser Phe Arg Glu Lys	
325 330	

<210> 2
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 <212> PRT

<213> Homo sapiens

<400> 2

Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala Ala Glu Ala Ala
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Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe Val Val
20 25 30

Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe Ser Leu
35 40 45

Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser Val Ser
50 55 60

Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser Tyr Ala
65 70 75 80

Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr
85 90 95

Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile
100 105 110

Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu His Leu
115 120 125

Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile Trp Val
130 135 140

Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn Pro Val
145 150 155 160

Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser Gly Asp
165 170 175

Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu Gly Phe
180 185 190

Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile Ala Leu
195 200 205

Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro Leu Glu
210 215 220

Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser Val Leu
 225 230 235 240

Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser Arg Leu
 245 250 255

Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn Ser Phe
 260 265 270

Tyr Ile Val Thr Arg Ala Leu Gly Phe Leu Asn Ser Val Ile Asn Pro
 275 280 285

Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu Met Asn
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Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg Trp Ala
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His Glu Leu Leu Leu Ser Phe Arg Glu Lys
 325 330

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:an artificially synthesized
 primer sequence

<400> 3
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<210> 4
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 <212> DNA
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 <223> Description of Artificial Sequence:an artificially synthesized
 primer sequence

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<400> 8
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<220>
 <223> Description of Artificial Sequence:an artificially synthesized
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<210> 10
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<220>
 <223> Description of Artificial Sequence:an artificially synthesized
 primer sequence

<400> 10
 ggaagatctt cctctcagcg gggaagag 28

<210> 11
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<220>
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 cactgctctt gtaatggaat cagacttctt attttaacaa gacaaaccaa atccaatcca 180
 catttgaaga ttatagggtt taatataaga aaatgcactc atttctcaaa gaccctagtg 240
 aagctgtgtt taaatgctcc taggtgaacc ccctttgcat ccagtggtc ccaccctgac 300
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Glu Tyr Asn Leu Val
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<210> 16
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Asp Cys Gly Leu Phe
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<210> 17
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<400> 17
 taccaatgac aacgcctcc

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<210> 18

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<400> 18
atgtcttcat gctggtgcag

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<210> 19
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<213> Homo sapiens

<400> 19
gggaaggtga aggtcgga

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<210> 20
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<213> Homo sapiens

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gcagccctgg tgaccag

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